

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/551,004
Source: Pt
Date Processed by STIC: 10/9/05

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>) , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05



PCT

RAW SEQUENCE LISTING

DATE: 10/07/2005

PATENT APPLICATION: US/10/551,004

TIME: 10:13:40

Input Set : A:\31098pw1.app

Output Set: N:\CRF4\10072005\J551004.raw

3 <110> APPLICANT: APOGENIX Biotechnology AG
 5 <120> TITLE OF INVENTION: Improved FC Fusion Proteins
 7 <130> FILE REFERENCE: 31098PWO-HC
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/551,004
 C--> 10 <141> CURRENT FILING DATE: 2005-09-26 *EP PCT/EP04/03239*
 12 <150> PRIOR APPLICATION NUMBER: PCT/2004/003239
 13 <151> PRIOR FILING DATE: 2004-03-26
 15 <160> NUMBER OF SEQ ID NOS: 82
 17 <170> SOFTWARE: PatentIn Ver. 2.1
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 30
 21 <212> TYPE: DNA
 22 <213> ORGANISM: Artificial Sequence
 24 <220> FEATURE:
 25 <223> OTHER INFORMATION: Description of Artificial Sequence: PCR primer
 26 for the amplification of CD95 cDNA
 28 <220> FEATURE:
 29 <223> OTHER INFORMATION: Sense huCD95-Hind III
 31 <400> SEQUENCE: 1
 32 tataaagctt gccaccatgc tgggcatctg 30
 35 <210> SEQ ID NO: 2
 36 <211> LENGTH: 27
 37 <212> TYPE: DNA
 38 <213> ORGANISM: Artificial Sequence
 40 <220> FEATURE:
 41 <223> OTHER INFORMATION: Description of Artificial Sequence: PCR primer for
 42 the amplification of CD95 cDNA
 44 <220> FEATURE:
 45 <223> OTHER INFORMATION: Antisense huCD95-BgI II
 47 <400> SEQUENCE: 2
 48 tataagatct ggatccttcc tctttgc 27
 51 <210> SEQ ID NO: 3
 52 <211> LENGTH: 30
 53 <212> TYPE: DNA
 54 <213> ORGANISM: Artificial Sequence
 56 <220> FEATURE:
 57 <223> OTHER INFORMATION: Description of Artificial Sequence: PCR primer
 58 for the amplification of IgG1 Fc cDNA
 60 <220> FEATURE:
 61 <223> OTHER INFORMATION: Sense hulg1Fc-BgIII
 63 <400> SEQUENCE: 3
 64 tataagatct tgtgacaaaa ctcacacatg 30
 67 <210> SEQ ID NO: 4

*Does Not Comply
Corrected Diskette Needed*

see p6, too

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68 <211> LENGTH: 30
69 <212> TYPE: DNA
70 <213> ORGANISM: Artificial Sequence
72 <220> FEATURE:
73 <223> OTHER INFORMATION: Description of Artificial Sequence: PCR primer for
74     the amplification of IgG1 Fc cDNA
76 <220> FEATURE:
77 <223> OTHER INFORMATION: Antisense hulgG1Fc-XhoI
79 <400> SEQUENCE: 4
80 tataactcgag tcattttaccc ggagacaggg                      30
83 <210> SEQ ID NO: 5
84 <211> LENGTH: 31
85 <212> TYPE: DNA
86 <213> ORGANISM: Artificial Sequence
88 <220> FEATURE:
89 <223> OTHER INFORMATION: Description of Artificial Sequence: PCR primer for
90     the changing the Kozak Sequence from GCCACCATGC to
91     GCCGCCACCATGG
93 <220> FEATURE:
94 <223> OTHER INFORMATION: ShuCD95EC_altKozak
96 <400> SEQUENCE: 5
97 tataaaagctt gccgccacca tgggtgggcat c                      31
100 <210> SEQ ID NO: 6
101 <211> LENGTH: 30
102 <212> TYPE: DNA
103 <213> ORGANISM: Artificial Sequence
105 <220> FEATURE:
106 <223> OTHER INFORMATION: Description of Artificial Sequence: PCR primer
107     for the changing the Kozak Sequence from
108     GCCACCATGC to GCCGCCACCATGG
110 <220> FEATURE:
111 <223> OTHER INFORMATION: AS698 hulgG1Fc-XhoI
113 <400> SEQUENCE: 6
114 tataactcgag tcattttaccc ggagacaggg                      30
117 <210> SEQ ID NO: 7
118 <211> LENGTH: 38
119 <212> TYPE: DNA
120 <213> ORGANISM: Artificial Sequence
122 <220> FEATURE:
123 <223> OTHER INFORMATION: Description of Artificial Sequence: primer for
124     amplifying cDNA of human IgG1 Fc (partial hinge
125     CH3)
127 <220> FEATURE:
128 <223> OTHER INFORMATION: Sense_hulgG1
130 <400> SEQUENCE: 7
131 ccaggggactc ctgcctcttg tgacaaaact cacacatg              38
134 <210> SEQ ID NO: 8
135 <211> LENGTH: 30
136 <212> TYPE: DNA

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TIME: 10:13:40

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137 <213> ORGANISM: Artificial Sequence
139 <220> FEATURE:
140 <223> OTHER INFORMATION: Description of Artificial Sequence: primer for
141     amplifying cDNA of human IgG1 Fc (partial hinge
142     CH3)
144 <220> FEATURE:
145 <223> OTHER INFORMATION: Antisense_ERIhulgG1
147 <400> SEQUENCE: 8
148 tatagaattc tcatttaccc ggagacaggg 30
151 <210> SEQ ID NO: 9
152 <211> LENGTH: 40
153 <212> TYPE: DNA
154 <213> ORGANISM: Artificial Sequence
156 <220> FEATURE:
157 <223> OTHER INFORMATION: Description of Artificial Sequence: primer used to
158     amplify the cDNA of TRAILR2 domain
160 <220> FEATURE:
161 <223> OTHER INFORMATION: Sense_HIII_TRAILR2
163 <400> SEQUENCE: 9
164 tataaagctt gccgccacca tggaacaacg gggacagaac 40
167 <210> SEQ ID NO: 10
168 <211> LENGTH: 33
169 <212> TYPE: DNA
170 <213> ORGANISM: Artificial Sequence
172 <220> FEATURE:
173 <223> OTHER INFORMATION: Description of Artificial Sequence: primer used to
174     amplify the cDNA of TRAILR2 domain
176 <220> FEATURE:
177 <223> OTHER INFORMATION: Antisense_TRAILR2
179 <400> SEQUENCE: 10
180 gtgagttttg tcacaagagg caggagtccc tgg 33
183 <210> SEQ ID NO: 11
184 <211> LENGTH: 40
185 <212> TYPE: DNA
186 <213> ORGANISM: Artificial Sequence
188 <220> FEATURE:
189 <223> OTHER INFORMATION: Description of Artificial Sequence: primer for PCR
190     used to utilize fragments for cloning purposes
192 <220> FEATURE:
193 <223> OTHER INFORMATION: Sense_HIII_TRAILR2
195 <400> SEQUENCE: 11
196 tataaagctt gccgccacca tggaacaacg gggacagaac 40
199 <210> SEQ ID NO: 12
200 <211> LENGTH: 30
201 <212> TYPE: DNA
202 <213> ORGANISM: Artificial Sequence
204 <220> FEATURE:
205 <223> OTHER INFORMATION: Description of Artificial Sequence: primer for
206     PCR used to utilize fragments for cloning

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207     purposes
209 <220> FEATURE:
210 <223> OTHER INFORMATION: Antisense_ERIhulgG1
212 <400> SEQUENCE: 12
213 tatagaattc tcatttaccc ggagacaggg                      30
216 <210> SEQ ID NO: 13
217 <211> LENGTH: 335
218 <212> TYPE: PRT
219 <213> ORGANISM: human
221 <220> FEATURE:
222 <223> OTHER INFORMATION: CD95 >sp/P25445/TNR6_HUMAN Tumor necrosis factor
223     receptor superfamily 6 precursor (FASL-receptor)
224     (Apoptosis-mediating surface antigen FAS) (Apo-1
225     antigen) (CD95) - Homo sapiens (Human)
227 <400> SEQUENCE: 13
228 Met Leu Gly Ile Trp Thr Leu Leu Pro Leu Val Leu Thr Ser Val Ala
229   1           5           10           15
231 Arg Leu Ser Ser Lys Ser Val Asn Ala Gln Val Thr Asp Ile Asn Ser
232           20           25           30
234 Lys Gly Leu Glu Leu Arg Lys Thr Val Thr Thr Val Glu Thr Gln Asn
235           35           40           45
237 Leu Glu Gly Leu His His Asp Gly Gln Phe Cys His Lys Pro Cys Pro
238           50           55           60
240 Pro Gly Glu Arg Lys Ala Arg Asp Cys Thr Val Asn Gly Asp Glu Pro
241           65           70           75           80
243 Asp Cys Val Pro Cys Gln Glu Gly Lys Glu Tyr Thr Asp Lys Ala His
244           85           90           95
246 Phe Ser Ser Lys Cys Arg Arg Cys Arg Leu Cys Asp Glu Gly His Gly
247           100          105          110
249 Leu Glu Val Glu Ile Asn Cys Thr Arg Thr Gln Asn Thr Lys Cys Arg
250           115          120          125
252 Cys Lys Pro Asn Phe Phe Cys Asn Ser Thr Val Cys Glu His Cys Asp
253           130          135          140
255 Pro Cys Thr Lys Cys Glu His Gly Ile Ile Lys Glu Cys Thr Leu Thr
256           145          150          155          160
258 Ser Asn Thr Lys Cys Lys Glu Glu Gly Ser Arg Ser Asn Leu Gly Trp
259           165          170          175
261 Leu Cys Leu Leu Leu Leu Pro Ile Pro Leu Ile Val Trp Val Lys Arg
262           180          185          190
264 Lys Glu Val Gln Lys Thr Cys Arg Lys His Arg Lys Glu Asn Gln Gly
265           195          200          205
267 Ser His Glu Ser Pro Thr Leu Asn Pro Glu Thr Val Ala Ile Asn Leu
268           210          215          220
270 Ser Asp Val Asp Leu Ser Lys Tyr Ile Thr Thr Ile Ala Gly Val Met
271           225          230          235          240
273 Thr Leu Ser Gln Val Lys Gly Phe Val Arg Lys Asn Gly Val Asn Glu
274           245          250          255
276 Ala Lys Ile Asp Glu Ile Lys Asn Asp Asn Val Gln Asp Thr Ala Glu
277           260          265          270

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DATE: 10/07/2005

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Input Set : A:\31098pw1.app

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```

279 Gln Lys Val Gln Leu Leu Arg Asn Trp His Gln Leu His Gly Lys Lys
280      275      280      285
282 Glu Ala Tyr Asp Thr Leu Ile Lys Asp Leu Lys Lys Ala Asn Leu Cys
283      290      295      300
285 Thr Leu Ala Glu Lys Ile Gln Thr Ile Ile Leu Lys Asp Ile Thr Ser
286 305      310      315      320
288 Asp Ser Glu Asn Ser Asn Phe Arg Asn Glu Ile Gln Ser Leu Val
289      325      330      335
293 <210> SEQ ID NO: 14
294 <211> LENGTH: 330
295 <212> TYPE: PRT
296 <213> ORGANISM: human
298 <220> FEATURE:
299 <223> OTHER INFORMATION: IgG1 > sp/P01857/GC1_HUMAN Ig gamma-1 chain C
300      region - Homo sapiens (Human)
302 <400> SEQUENCE: 14
303 Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
304 1      5      10      15
306 Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
307      20      25      30
309 Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
310      35      40      45
312 Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
313      50      55      60
315 Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
316 65      70      75      80
318 Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
319      85      90      95
321 Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
322      100     105     110
324 Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
325      115     120     125
327 Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
328      130     135     140
330 Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
331 145     150     155     160
333 Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
334      165     170     175
336 Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
337      180     185     190
339 His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
340      195     200     205
342 Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
343      210     215     220
345 Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
346 225     230     235     240
348 Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
349      245     250     255
351 Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn

```

<210> 19
<211> 468
<212> PRT
<213> human

<220>

<223> TRAIL-R1 >sp/000220/T10A HUMAN Tumor necrosis
factor receptor superfamily member 10A precursor
(Death receptor 4) (TNF-related

<220> ~~apoptosis-including ligand receptor 1) (TRAIL~~
<223> receptor-1) (TRAIL-R1)

<400> 19

Per 1.823 of Sequence
Rule, a MAXIMUM
of 4 lines for
<223> response.

Please insert a
<220> above fifth
line and a <223>
at beginning of fifth
line

IMPORTANT

The types of errors shown exist throughout
the Sequence Listing. Please check subsequent
sequences for similar errors.

The above is a sample of a global error.

VERIFICATION SUMMARYPATENT APPLICATION: **US/10/551,004**

DATE: 10/07/2005

TIME: 10:13:41

Input Set : **A:\31098pw1.app**Output Set: **N:\CRF4\10072005\J551004.raw**

L:9 M:270 C: Current Application Number differs, Replaced Current Application Number
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:540 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:781 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:901 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:908 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:938 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:968 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:998 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:1028 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:1058 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:1106 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:1133 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:1160 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:1187 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:1211 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:1461 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:1551 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:1581 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:1611 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:1641 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:1671 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:1698 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:1746 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:1776 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:1806 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:1836 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:1866 M:259 W: Allowed number of lines exceeded, <223> Other Information: